

amino acid sequenceX-(Cys<sup>41</sup>-Cys<sup>133</sup>)-Ywherein(Cys<sup>41</sup>-Cys<sup>133</sup>) consists of Cys<sup>41</sup> through Cys<sup>133</sup> of SEQ ID NO:2;Y represents the carboxy terminal group of Cys<sup>133</sup>, a carboxy-terminus amino acid residue of Ile<sup>134</sup>, or a substituted amino acid residue, andX represents a methionylated or nonmethionylated amine group of Cys<sup>41</sup> or amino-terminus amino acid residue(s) selected from the group:

G  
 RG  
 NRG  
KNRG (SEQ ID NO:3)  
GKNRG (SEQ ID NO:4)  
RGKNRG (SEQ ID NO:5)  
ORGKNRG (SEQ ID NO:6)  
GORGKNRG (SEQ ID NO:7)  
RGORGKNRG (SEQ ID NO:8)  
RRGORGKNRG (SEQ ID NO:9)  
G RRGORGKNRG (SEQ ID NO:10)  
KG RRGORGKNRG (SEQ ID NO:11)  
GKG RRGORGKNRG (SEQ ID NO:12)  
RGKG RRGORGKNRG (SEQ ID NO:13)  
SRGKG RRGORGKNRG (SEQ ID NO:14)  
NSRGKG RRGORGKNRG (SEQ ID NO:15)  
ENSRGKG RRGORGKNRG (SEQ ID NO:16)  
PENSRGKG RRGORGKNRG (SEQ ID NO:17)  
NPENSRGKG RRGORGKNRG (SEQ ID NO:18)  
ANPENSRGKG RRGORGKNRG (SEQ ID NO:19)  
A ANPENSRGKG RRGORGKNRG (SEQ ID NO:20)  
AA ANPENSRGKG RRGORGKNRG (SEQ ID NO:21)  
AAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:22)  
QQAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:23)  
ROAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:24)  
NROAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:25)

RNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:26)  
 ERNROAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:27)  
 RERNROAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:28)  
 RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:29)  
 P RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:30)  
 LP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:31)  
 VLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:32)  
 AVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:33)  
 MAVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:34)  
 QMAVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:35)  
 KOMAVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:36)  
 DKOMAVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:37) and  
 PDKOMAVLP RRERNRQAAA ANPENSRGKG RRGORGKNRG (SEQ ID NO:38)

or a substitution or deletion variant of X, wherein said variant is in excess of 70% identical to an amino acid sequence of X as set forth above when four gaps in a length of 100 amino acids may be introduced to assist in that alignment, to provide *in vivo* production of said truncated GDNF protein.

32. (Amended) A method according to claim 31 [of treating Parkinson's Disease] comprising implanting in a patient a cell transformed with said [a] polynucleotide [sequence of Claim 13] to provide *in vivo* production of said truncated GDNF protein.

Please add the following new claims:

-- 45. A method according to Claim 31 or 32, wherein X is selected from the group consisting of

SEQ ID NO: 3, 7, 8, 14, 17 and 18.

46. A method according to Claim 31 or 32, wherein X is G, RG or NRG.

47. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:42.

*Sub B1  
P3  
C9*

48. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:44.

49. A method according to Claim 31 or 32, wherein said GDNF protein product has the amino acid sequence of SEQ ID NO:46. --

Respectfully submitted,

*Daniel R. Curry*

Daniel R. Curry  
Attorney for Applicant  
Registration No.: 32,727  
Phone: (805) 447-8102  
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Please send all future correspondence to:

U.S. Patent Operations/ DRC  
Dept. 4300, M/S 27-4-A  
AMGEN INC.  
One Amgen Center Drive  
Thousand Oaks, California 91320-1799